O280

RAW SEQUENCE LISTING   DATE: 10/27/2000
PATENT APPLICATION: US/09/686,499   TIME: 08:23:56

Input Set : A:\31161192.app
Output Set: N:\CRF3\10272000\I686499.raw

```
     3 <110> APPLICANT: CURTISS III, Roy
     5 <120> TITLE OF INVENTION: FUNCTIONAL BALANCED-LETHAL HOST-VECTOR SYSTEMS
     7 <130> FILE REFERENCE: 3116-1192
C--> 9 <140> CURRENT APPLICATION NUMBER: US/09/686,499
C--> 10 <141> CURRENT FILING DATE: 2000-10-11
     12 <160> NUMBER OF SEQ ID NOS: 8
     14 <170> SOFTWARE: PatentIn Ver. 2.0
     16 <210> SEQ ID NO: 1
     17 <211> LENGTH: 1735
     18 <212> TYPE: DNA
     19 <213> ORGANISM: Salmonella typhimurium
     21 <400> SEQUENCE: 1
     22 ggatcttccc taaatttaaa tataaacaac gaattatctc cttaacgtac gttttcgttc 60
     23 cattggccct caaaccccta attaggatca ataaaacagc gacggaaatg attcccttcc 120
     24 taacgcaaat tccctgataa tcgccactgg actttctgct tgcgcggtaa ggcaggataa 180
     25 gtcgcattac tgatggcttc gctatcattg attaatttca cttgcgactt tggctgcttt 240
     26 ttgtatggtg aaggatgcgc cacaggatac tggcgcgcat acacagcaca tctctttgca 300
     27 ggaaaaaaac gctatgaaaa atgttggttt tatcggctgg cgcggaatgg tcggctctgt 360
     28 tctcatgcaa cgcatggtag aggagcgcga tttcgacgct attcgccctg ttttcttttc 420
     29 tacctcccag tttggacagg cggcgcccac cttcggcgac acctccaccg gcacgctaca 480
     30 ggacgctttt gatctggatg cgctaaaagc gctcgatatc atcgtgacct gccagggcgg 540
     31 cgattatacc aacgaaattt atccaaagct gcgcgaaagc ggatggcagg gttactggat 600
     32 tgatgcggct tctacgctgc gcatgaaaga tgatgccatt attattctcg acccggtcaa 660
     33 ccaggacgtg attaccgacg gcctgaacaa tggcgtgaag acctttgtgg gcggtaactg 720
     34 taccgttagc ctgatgttga tgtcgctggg cggtctcttt gcccataatc tcgttgactg 780
     35 ggtatccgtc gcgacctatc aggccgcctc cggcggcggc gcgcgccata tgcgcgagct 840
     36 gttaacccag atgggtcagt tgtatggcca tgtcgccgat gaactggcga cgccgtcttc 900
     37 cgcaattctt gatattgaac gcaaagttac ggcattgacc cgcagcggcg agctgccggt 960
     38 tgataacttt ggcgtaccgc tggcgggaag cctgatcccc tggatcgaca aacagctcga 1020
     39 taacggccag agccgcgaag agtggaaagg ccaggcggaa accaacaaga ttctcaatac 1080
     40 tgcctctgtg attccggttg atggtttgtg tgtgcgcgtc ggcgcgctgc gctgtcacag 1140
     41 ccaggcgttc accatcaagc tgaaaaaaga ggtatccatt ccgacggtgg aagaactgct 1200
     42 ggcggcacat aatccgtggg cgaaagtggt gccgaacgat cgtgatatca ctatgcgcga 1260
     43 attaaccccg gcggcggtga ccggcacgtt gactacgccg gttggtcgtc tgcgtaagct 1320
     44 gaacatgggg ccagagttct tgtcggcgtt taccgtaggc gaccagttgt tatggggcgc 1380
     45 cgccgagccg ctgcgtcgaa tgctgcgcca gttggcgtag tggctattgc agcgcttatc 1440
     46 gggcctgcgt gtggttctgt aggccggata aggcgcgtca gcgccgccat ccggcgggga 1500
     47 aatttgtgtt aaaccagggg tgcatcgtca cccttttttt gcgtaataca ggagtaaacg 1560
     48 cagatgtttc atttttatca ggagttaagc agagcattgg ctattcttta agggtagctt 1620
     49 aatcccacgg gtattaagcc taacctgaag gtaggacgac gcagatagga tgcacagtgt 1680
     50 gctgcgccgt tcaggtcaaa gaagtgtcac tacctgatgt tgaattggaa gatcc      1735
     52 <210> SEQ ID NO: 2
     53 <211> LENGTH: 391
     54 <212> TYPE: PRT
     55 <213> ORGANISM: Salmonella typhimurium
     57 <400> SEQUENCE: 2
     58 Met Val Lys Asp Ala Pro Gln Asp Thr Gly Ala His Thr Gln His Ile
```

```
            Input Set : A:\31161192.app
            Output Set: N:\CRF3\10272000\I686499.raw

 59   1                      5                  10                  15
 61 Ser Leu Gln Glu Lys Asn Ala Met Lys Asn Val Gly Phe Ile Gly Trp
 62             20                  25                  30
 64 Arg Gly Met Val Gly Ser Val Leu Met Gln Arg Met Val Glu Glu Arg
 65         35                  40                  45
 67 Asp Phe Asp Ala Ile Arg Pro Val Phe Phe Ser Thr Ser Gln Phe Gly
 68     50                  55                  60
 70 Gln Ala Ala Pro Thr Phe Gly Asp Thr Ser Thr Gly Thr Leu Gln Asp
 71 65                  70                  75                  80
 73 Ala Phe Asp Leu Asp Ala Leu Lys Ala Leu Asp Ile Ile Val Thr Cys
 74                 85                  90                  95
 76 Gln Gly Gly Asp Tyr Thr Asn Glu Ile Tyr Pro Lys Leu Arg Glu Ser
 77             100                 105                 110
 79 Gly Trp Gln Gly Tyr Trp Ile Asp Ala Ala Ser Thr Leu Arg Met Lys
 80         115                 120                 125
 82 Asp Asp Ala Ile Ile Ile Leu Asp Pro Val Asn Gln Asp Val Ile Thr
 83     130                 135                 140
 85 Asp Gly Leu Asn Asn Gly Val Lys Thr Phe Val Gly Gly Asn Cys Thr
 86 145                 150                 155                 160
 88 Val Ser Leu Met Leu Met Ser Leu Gly Gly Leu Phe Ala His Asn Leu
 89                 165                 170                 175
 91 Val Asp Trp Val Ser Val Ala Thr Tyr Gln Ala Ala Ser Gly Gly Gly
 92             180                 185                 190
 94 Ala Arg His Met Arg Glu Leu Leu Thr Gln Met Gly Gln Leu Tyr Gly
 95         195                 200                 205
 97 His Val Ala Asp Glu Leu Ala Thr Pro Ser Ser Ala Ile Leu Asp Ile
 98     210                 215                 220
100 Glu Arg Lys Val Thr Ala Leu Thr Arg Ser Gly Glu Leu Pro Val Asp
101 225                 230                 235                 240
103 Asn Phe Gly Val Pro Leu Ala Gly Ser Leu Ile Pro Trp Ile Asp Lys
104             245                 250                 255
106 Gln Leu Asp Asn Gly Gln Ser Arg Glu Glu Trp Lys Gly Gln Ala Glu
107             260                 265                 270
109 Thr Asn Lys Ile Leu Asn Thr Ala Ser Val Ile Pro Val Asp Gly Leu
110     275                 280                 285
112 Cys Val Arg Val Gly Ala Leu Arg Cys His Ser Gln Ala Phe Thr Ile
113     290                 295                 300
115 Lys Leu Lys Lys Glu Val Ser Ile Pro Thr Val Glu Glu Leu Leu Ala
116 305                 310                 315                 320
118 Ala His Asn Pro Trp Ala Lys Val Val Pro Asn Asp Arg Asp Ile Thr
119             325                 330                 335
121 Met Arg Glu Leu Thr Pro Ala Ala Val Thr Gly Thr Leu Thr Thr Pro
122             340                 345                 350
124 Val Gly Arg Leu Arg Lys Leu Asn Met Gly Pro Glu Phe Leu Ser Ala
125         355                 360                 365
127 Phe Thr Val Gly Asp Gln Leu Leu Trp Gly Ala Ala Glu Pro Leu Arg
128     370                 375                 380
130 Arg Met Leu Arg Gln Leu Ala
131 385                 390
```

Input Set : A:\31161192.app
Output Set: N:\CRF3\10272000\I686499.raw

```
134 <210> SEQ ID NO: 3
135 <211> LENGTH: 1961
136 <212> TYPE: DNA
137 <213> ORGANISM: Salmonella typhimurium and Pseudomonas putida
139 <400> SEQUENCE: 3
140 ggatcttccc taaatttaaa tataaacaac gaattatctc cttaacgtac gttttcgttc 60
141 cattggccct caaacccta attaggatca ataaaacagc gacggaaatg attcccttcc 120
142 taacgcaaat tccctgataa tcgccactgg actttctgct tgcgcggtaa ggcaggataa 180
143 gtcgcattac tgatggcttc gctatcattg attaatttca cttgcgactt tggctgcttt 240
144 ttgtatggtg aaggatgcgc cacaggatac tggcgcgcat acacagcaca tctctttgca 300
145 ggaaaaaaac gctatgaaaa atgttggttt tatcggctgg cgcggaatgg tcggctctgt 360
146 tctcatgcaa cgcatggtag aggagcgcga tttcgacgct attcgccctg ttttctttc 420
147 tacctcccag tttggacagg cggcgcccac cttcggcgac acctccaccg gcacgctaca 480
148 ggacgctttt gatctggatg cgctaaaagc gctcgatgat ctatgaagag gtgacgtcat 540
149 gaacaaaggt gtaatgcgac cgggccatgt gcagctgcgt gtactggaca tgagcaaggc 600
150 cctggaacac tacgtcgagt tgctgggcct gatcgagatg gaccgtgacg accagggccg 660
151 tgtctatctg aaggcttgga ccgaagtgga taagtttccc ctggtgctac gcgaggctga 720
152 cgagccgggc atggattta tgggtttcaa ggttgtggat gaggatgctc tccggcaact 780
153 ggagcgggat ctgatggcat atggctgtgc cgttgagcag ctacccgcag gtgaactgaa 840
154 cagttgtggc cggcgcgtgc gttccaggcc ctccgggcat cacttcgagt tgtatgcaga 900
155 caaggaatat actggaaagt ggggtttgaa tgacgtcaat cccgaggcat ggccgcgcga 960
156 tctgaaaggt atggcggctg tgcgtttcga ccacgccctc atgtatggcg acgaattgcc 1020
157 ggcgacctat gacctgttca ccaaggtgct cggtttctat ctggccgaac aggtgcttgga 1080
158 cgaaaatggc acgcgcgtcg cccagtttct cagtctgtcg accaaggccc acgacgtggc 1140
159 cttcattcac catccggaaa aaggccgcct ccatcatgtg tccttccacc tcgaaacctg 1200
160 ggaagacttg cttcgcgccg ccgacctgat ctccatgacc gacacatcta tcgatatcgg 1260
161 cccaacccgc cacggcctca ctcacggcaa gaccatctac ttcttcgacc cgtccggtaa 1320
162 ccgcaacgaa gtgttctgcg ggggagatta caactacccg gaccacaaac cggtgacctg 1380
163 gaccaccgac cagctgggca aagccttctt ttaccacgac cgcattctca acgaacgatt 1440
164 catgaccgtg ctgacctgat ggtccggaga tcatcactat gcgcgaatta accccggcgg 1500
165 cggtgaccgg cacgttgact acgccggttg gtcgtctgcg taagctgaac atggggccag 1560
166 agttcttgtc ggcgtttacc gtaggcgacc agttgttatg gggcgccgcc gagccgctgc 1620
167 gtcgaatgct gcgccagttg gcgtagtggc tattgcagcg cttatcgggc ctgcgtgtgg 1680
168 ttctgtaggc cggataaggc gcgtcagcgc cgccatccgg cggggaaatt tgtgttaaac 1740
169 cagggggtgca tcgtcaccct tttttttgcgt aatacaggag taaacgcaga tgtttcattt 1800
170 ttatcaggag ttaagcagag cattggctat tctttaaggg tagcttaatc ccacgggtat 1860
171 taagcctaac ctgaaggtag gacgacgcag ataggatgca cagtgtgctg cgccgttcag 1920
172 gtcaaagaag tgtcactacc tgatgttgaa ttggaagatc c                      1961
174 <210> SEQ ID NO: 4
175 <211> LENGTH: 454
176 <212> TYPE: PRT
177 <213> ORGANISM: Salmonella typhimurium and Pseudomonas putida
179 <400> SEQUENCE: 4
180 Met Val Lys Asp Ala Pro Gln Asp Thr Gly Ala His Thr Gln His Ile
181   1               5                  10                  15
183 Ser Leu Gln Glu Lys Asn Ala Met Lys Asn Val Gly Phe Ile Gly Trp
184              20                  25                  30
186 Arg Gly Met Val Gly Ser Val Leu Met Gln Arg Met Val Glu Glu Arg
187          35                  40                  45
```

```
189 Asp Phe Asp Ala Ile Arg Pro Val Phe Phe Ser Thr Ser Gln Phe Gly
190      50              55              60
192 Gln Ala Ala Pro Thr Phe Gly Asp Thr Ser Thr Gly Thr Leu Gln Asp
193 65              70              75                      80
195 Ala Phe Asp Leu Asp Ala Leu Lys Ala Leu Asp Met Asn Lys Gly Val
196              85              90                      95
198 Met Arg Pro Gly His Val Gln Leu Arg Val Leu Asp Met Ser Lys Ala
199          100             105             110
201 Leu Glu His Tyr Val Glu Leu Leu Gly Leu Ile Glu Met Asp Arg Asp
202          115             120             125
204 Asp Gln Gly Arg Val Tyr Leu Lys Ala Trp Thr Glu Val Asp Lys Phe
205      130             135             140
207 Ser Leu Val Leu Arg Glu Ala Asp Glu Pro Gly Met Asp Phe Met Gly
208 145             150             155             160
210 Phe Lys Val Val Asp Glu Asp Ala Leu Arg Gln Leu Glu Arg Asp Leu
211              165             170             175
213 Met Ala Tyr Gly Cys Ala Val Glu Gln Leu Pro Ala Gly Glu Leu Asn
214          180             185             190
216 Ser Cys Gly Arg Arg Val Arg Ser Arg Pro Ser Gly His His Phe Glu
217          195             200             205
219 Leu Tyr Ala Asp Lys Glu Tyr Thr Gly Lys Trp Gly Leu Asn Asp Val
220      210             215             220
222 Asn Pro Glu Ala Trp Pro Arg Asp Leu Lys Gly Met Ala Ala Val Arg
223 225             230             235             240
225 Phe Asp His Ala Leu Met Tyr Gly Asp Glu Leu Pro Ala Thr Tyr Asp
226              245             250             255
228 Leu Phe Thr Lys Val Leu Gly Phe Tyr Leu Ala Glu Gln Val Leu Asp
229          260             265             270
231 Glu Asn Gly Thr Arg Val Ala Gln Phe Leu Ser Leu Ser Thr Lys Ala
232          275             280             285
234 His Asp Val Ala Phe Ile His His Pro Glu Lys Gly Arg Leu His His
235      290             295             300
237 Val Ser Phe His Leu Glu Thr Trp Glu Asp Leu Leu Arg Ala Ala Asp
238 305             310             315             320
240 Leu Ile Ser Met Thr Asp Thr Ser Ile Asp Ile Gly Pro Thr Arg His
241              325             330             335
243 Gly Leu Thr His Gly Lys Thr Ile Tyr Phe Phe Asp Pro Ser Gly Asn
244          340             345             350
246 Arg Asn Glu Val Phe Cys Gly Gly Asp Tyr Asn Tyr Pro Asp His Lys
247          355             360             365
249 Pro Val Thr Trp Thr Thr Asp Gln Leu Gly Lys Ala Phe Phe Tyr His
250      370             375             380
252 Asp Arg Ile Leu Asn Glu Arg Phe Met Thr Val Leu Thr Ile Thr Met
253 385             390             395             400
255 Arg Glu Leu Thr Pro Ala Ala Val Thr Gly Thr Leu Thr Thr Pro Val
256              405             410             415
258 Gly Arg Leu Arg Lys Leu Asn Met Gly Pro Glu Phe Leu Ser Ala Phe
259          420             425             430
261 Thr Val Gly Asp Gln Leu Leu Trp Gly Ala Ala Glu Pro Leu Arg Arg
```

```
262          435                    440                    445
264 Met Leu Arg Gln Leu Ala
265      450
268 <210> SEQ ID NO: 5
269 <211> LENGTH: 91
270 <212> TYPE: PRT
271 <213> ORGANISM: Salmonella typhimurium
273 <400> SEQUENCE: 5
274 Met Val Lys Asp Ala Pro Gln Asp Thr Gly Ala His Thr Gln His Ile
275   1               5                  10                     15
277 Ser Leu Gln Glu Lys Asn Ala Met Lys Asn Val Gly Phe Ile Gly Trp
278              20                  25                     30
280 Arg Gly Met Val Gly Ser Val Leu Met Gln Arg Met Val Glu Glu Arg
281          35                  40                  45
283 Asp Phe Asp Ala Ile Arg Pro Val Phe Phe Ser Thr Ser Gln Phe Gly
284      50                  55                  60
286 Gln Ala Ala Pro Thr Phe Gly Asp Thr Ser Thr Gly Thr Leu Gln Asp
287  65                  70                  75                  80
289 Ala Phe Asp Leu Asp Ala Leu Lys Ala Leu Asp
290              85                  90
293 <210> SEQ ID NO: 6
294 <211> LENGTH: 306
295 <212> TYPE: PRT
296 <213> ORGANISM: Pseudomonas putida
298 <400> SEQUENCE: 6
299 Met Asn Lys Gly Val Met Arg Pro Gly His Val Gln Leu Arg Val Leu
300  1               5                  10                     15
302 Asp Met Ser Lys Ala Leu Glu His Tyr Val Glu Leu Leu Gly Leu Ile
303              20                  25                     30
305 Glu Met Asp Arg Asp Asp Gln Gly Arg Val Tyr Leu Lys Ala Trp Thr
306          35                  40                  45
308 Glu Val Asp Lys Phe Ser Leu Val Leu Arg Glu Ala Asp Glu Pro Gly
309      50                  55                  60
311 Met Asp Phe Met Gly Phe Lys Val Val Asp Glu Asp Ala Leu Arg Gln
312  65              70                  75                     80
314 Leu Glu Arg Asp Leu Met Ala Tyr Gly Cys Ala Val Glu Gln Leu Pro
315              85                  90                     95
317 Ala Gly Glu Leu Asn Ser Cys Gly Arg Arg Val Arg Ser Arg Pro Ser
318              100                 105                 110
320 Gly His His Phe Glu Leu Tyr Ala Asp Lys Glu Tyr Thr Gly Lys Trp
321          115                 120                 125
323 Gly Leu Asn Asp Val Asn Pro Glu Ala Trp Pro Arg Asp Leu Lys Gly
324      130                 135                 140
326 Met Ala Ala Val Arg Phe Asp His Ala Leu Met Tyr Gly Asp Glu Leu
327 145              150                 155                 160
329 Pro Ala Thr Tyr Asp Leu Phe Thr Lys Val Leu Gly Phe Tyr Leu Ala
330              165                 170                 175
332 Glu Gln Val Leu Asp Glu Asn Gly Thr Arg Val Ala Gln Phe Leu Ser
333              180                 185                 190
```

VERIFICATION SUMMARY
PATENT APPLICATION: US/09/686,499

DATE: 10/27/2000
TIME: 08:23:58

Input Set : A:\31161192.app
Output Set: N:\CRF3\10272000\I686499.raw

L:9 M:270 C: Current Application Number differs, Replaced Application Number
L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date